

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Peter Ruhdal Jensen
- (B) STREET: Soegaardsvej 19
- (C) CITY: Gentofte
- (E) COUNTRY: Denmark
- (F) POSTAL CODE (ZIP): DK-2820

(ii) TITLE OF INVENTION: Artificial promoter libraries for selected organisms and promoters derived from such libraries

(iii) NUMBER OF SEQUENCES: 58

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: DK 886/96
- (B) FILING DATE: 23-AUG-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 26..82
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Artificial promoter library"
/note= "A degenerated sequence specifying a mixture of artificial promoters covering a wide range of expression in small steps in L. lactis"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 31..45
- (D) OTHER INFORMATION: /standard_name= "Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

- (B) LOCATION:60..69
- (D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:74..82
- (D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: -35_signal
- (B) LOCATION:40..45
- (D) OTHER INFORMATION:/standard_name= "-35 box"

(ix) FEATURE:

- (A) NAME/KEY: -10_signal
- (B) LOCATION:63..68
- (D) OTHER INFORMATION:/standard_name= "Pribnow box"

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION:3..25
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
/standard_name= "Multiple cloning site"
/label= MCS
/note= "A sequence specifying recognition sites for the restriction endonucleases: NlaIV, BstYI, BamHI, AlwI, MboI, DpnI, AflII, MseI, SspI, NsiI."

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION:74..98
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
/standard_name= "Multiple cloning site"
/label= MCS
/note= "A sequence specifying recognition sites for the restriction endonucleases: ScaI, RsaI, HpaI, HincII, MseI, SfcI, PstI, Fnu4HI, BbvI, PvuII, NspBII, AluI, EcoRI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
CGGGATCCTT AAGAATATTA TGCATNNNNN AGTTTATTCT TGACANNNNN NNNNNNNNT      60
GGTATAATAN NANAGTACTG TTAAGTGCAG CTGAATTCGG                             100
```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:23..95
- (D) OTHER INFORMATION:/standard_name= "Artificial promoter library"
/note= "A degenerated sequence specifying a mixture of artificial temperature regulated promoters covering a wide range of expression in small steps in *L. lactis*"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:23..49
- (D) OTHER INFORMATION:/standard_name= "Sequence providing temperature regulation to promoters"
/note= "This sequence comprising two inverted repeats separated by a short spacer provides temperature (heat shock) regulation to promoters in Gram-positive bacteria"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:50..60
- (D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:75..84
- (D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:89..95
- (D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: -35_signal
- (B) LOCATION:55..60
- (D) OTHER INFORMATION:/standard_name= "-35 box"

(ix) FEATURE:

- (A) NAME/KEY: -10_signal
- (B) LOCATION:78..83
- (D) OTHER INFORMATION:/standard_name= "Pribnow box"

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION:3..22
- (D) OTHER INFORMATION:/standard_name= "Multiple cloning site"
/label= MCS
/note= "A sequence specifying recognition sites for the restriction endonucleases: *Nla*IV, *Bst*YI, *Bam*HI, *Alu*I, *Mbo*I, *Dpn*I, *Hind*III, *Alu*I, *Mse*I (2 sites), *Ssp*I, *Ase*I."

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION:89..111
- (D) OTHER INFORMATION:/standard_name= "Multiple cloning site"
/label= MCS
/note= "A sequence specifying recognition sites for the

restriction endonucleases: ScaI, RsaI, SfcI, PstI, Fnu4HI, BbvI, PvuII, NspBII, AluI, XbaI, MaeI, EcoRI, ApoI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
CGGGATCCAA GCTTAATATT AATTAGCACT C>NNNNNNNNN GAGTGCTAAT TTTTGTGACA      60
NNNNNNNNNN NNNNTGGTAT AATANNANAG TACTGCAGCT GTCTAGAATT CGG              113
```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION:10..16
- (D) OTHER INFORMATION:/function= "Activating promoters in *S. cerevisiae*"
/bound_moiety= "GCN4 protein"
/standard_name= "Upstream activating sequence"
/label= UAS_GC4p
/note= "A DNA sequence that specifies a binding site for the GCN4 protein, which activates the transcription of genes involved in aminoacid synthesis in *S. cerevisiae*."

(ix) FEATURE:

- (A) NAME/KEY: TATA_signal
- (B) LOCATION:67..72
- (D) OTHER INFORMATION:/standard_name= "TATA box"

(ix) FEATURE:

- (A) NAME/KEY: misc_signal
- (B) LOCATION:122..144
- (D) OTHER INFORMATION:/function= "Transcription initiation"
/standard_name= "TI box"

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION:122..144
- (D) OTHER INFORMATION:/bound_moiety= "Arginine repressor"
/standard_name= "arginine repressor binding site"
/label= argR

(ix) FEATURE:

- (A) NAME/KEY: misc_RNA
- (B) LOCATION:145..192
- (D) OTHER INFORMATION:/function= "Spacer"
/standard_name= "Part of native sequence for ARG8"

gene incl. first codon"

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION:3..8
- (D) OTHER INFORMATION:/standard_name= "Recognition site
for restriction endonuclease EcoRI"
/label= EcoRI_site

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION:192..197
- (D) OTHER INFORMATION:/standard_name= "Recognition site
for restriction endonuclease BamHI"
/label= BamHI_site

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:10..192
- (D) OTHER INFORMATION:/standard_name= "Artificial
promoter library"
/note= "A degenerated sequence specifying a mixture of
artificial promoters covering a wide range of expression
in small steps in *S. cerevisiae*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGAAATTCGT GACTCANNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	60
NNNNNNNNNN NNNNNNTATA AANNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	120
NCTCTTAAGT GCAAGTGACT GCGAACATTT TTTTCGTTTG TTAGAATAAT TCAAGAATCG	180
CTACCAATCA TGGATCCCCG	199

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:1..45
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
/standard_name= "Artificial promoter library"
/note= "A degenerated sequence specifying a mixture of
artificial promoters covering a wide range of expression
in small steps in *Pseudomonas putida*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

NNNNNNNNNTT GRNNNNNNNNN NNNNNNNNNN NTATRATNNN NNNNN

45

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CATACCGGAG TTTATTCTTG ACAGTTCAC CTCGGGTGA TATAATATCT CAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CATGGCTTAG TTTATTCTTG ACAGGGTAGT ATCACTGTGA TATAATAGGA CAGTACTGTT

60

Sequence 45-60

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Lactococcus lactis
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION: 4..59
 - (D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp11
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CATAAGTGAG TTTATTCTTG ACCCGGACGC CCCCCTTGA TATAATAAGT AGTACTGTT

59

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Lactococcus lactis
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION: 4..60
 - (D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp12
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CATATACAAG TTTATTCTTG AACTAGTCG GCCAAAATGA TATAATACCT GAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard_name= "Constitutional
promoter"
/label= Cp13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CATGCTTTAC TTTATTCTTG ACAAACCAC CAGCTTTTGG TATAATACGT GAGAACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard_name= "Constitutional
promoter"
/label= Cp14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CATGACGGAG TTTATTCTTG ACACAGGTAT GGACTTATGA TATAATAAAA CAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard_name= "Constitutional
promoter"
/label= Cp15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CATTACNTAG TTNATTCTTG ACAGAATTAC GATTCGCTGG TATAATATAT CAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..58

(D) OTHER INFORMATION: /standard_name= "Constitutional
promoter"
/label= Cp16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CATTGTGTAG TTTATTCTTG ACAGCTATGA GTCAATTGG TATAATAACA GTACTCAG

58

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..59

(D) OTHER INFORMATION: /standard_name= "Constitutional
promoter"
/label= Cp17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CATTCTGGAG TTTATTCTTG ACCGCTCAGT ATGCAGTGGT ATAATAGTAC AGTACTGTT

59

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..58

(D) OTHER INFORMATION: /standard_name= "Constitutional
promoter"
/label= Cp18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CATTTTGCAG TTTATTCTTG ACATTGTGTG CTTCGGGTGT ATAATACTAA GTACTGTT

58

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..58

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CATCGCTTAG TTTTCTTGA CAGGAGGGAT CCGGGTTGAT ATAATAGTTA GTACTGTT

58

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..60
- (D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CATTGCTAG TTTATTCTTG ACATGAAGCG TGCCTAATGG TATATTACTT GAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..60
- (D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CATGGGTGAG TTTATTCTTG ACAGTGC GGC CNGGGGCTGA TATCATAGCA GAGTACTATT 60

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..59
- (D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CATTACCGAG TTTATTCTTG ACACCGTTTA TCGGGGTTGT ATAATACTAT AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CATGTAGGAG TTTATTCTTG ACAGATTAGT TAGGGGGTGG TATAATATCT CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CATGGGTAAG TTTATTCTTC ACACTATCTG GGCCCGATGG TATAATAAGT GACTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 3..59
- (D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTTTGGCAGT TTATTCTTGA CATGTAGTGA GGGGGCTGGT ATAATCACAT AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: YES
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Lactococcus lactis
(ix) FEATURE:
 (A) NAME/KEY: promoter
 (B) LOCATION: 4..60
 (D) OTHER INFORMATION: /standard_name= "Constitutional
 promoter"
 /label= Cp26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CATTCTACAG TTTATTCTTG ACATTGCACT GTCCCCCTGG TATAATAACT ATACATGCAT 60

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: YES
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
 (A) NAME/KEY: promoter
 (B) LOCATION: 4..60
 (D) OTHER INFORMATION: /standard_name= "Constitutional
 promoter"
 /label= Cp28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CATGGGGCCG TTTATTCTTG ACAACGGCGA GCAGACCTGG TATAATAATA TAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..59

(D) OTHER INFORMATION: /standard_name= "Constitutional
promoter"
/label= Cp29

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CATCGGTAAG TTATTCTTGA CATCTCAGGG GGGACGTGGT ATAATAACTG AGTACTGTT

59

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard_name= "Constitutional
promoter"
/label= Cp3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CATCCTGTAG TTTATTCTTG ACACACGTNN TTAGCTGTGG TATAATAGGA GAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CATGACAGAG TTTATTCTTG ACAGTATTGG GTTACTTTGG TATAATAGTT GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CATACGGGAG TTTATTCTTG ACATATTGCC GGTGTGTTGG TATAATAACT TAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CATGTTGGAG TTTATTCTTG ACATACAATT ACTGCAGTGA TATAATAGGT GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..60
- (D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CATCGCGAAG TTTATTCTTC ACACACCGCA GAACTTGTGG TATAATACAA CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..59
- (D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CATCATTAAG TTTATTCTTC ACATTGGCCG GAATTGTTGT ATAATACCTT AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CATAGAGAAG TTTATTCTTG ACAGCTAACT TGGCCTTTGA TATAATACAT GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CATTGCGAAG TTTATTCTTG ACAGTACGTT TTTACCATGA TATAATAGTA TAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GATGTTTTAG TTTATTCTTG ACACCGTATC GTGCGCGTGA TATAATCGGG ATCCTTAAGA 60

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CATAGAACAG TTTATTCTTG ACATTGAATA AGAAGGCTGA TATAATAGCC AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..59

(D) OTHER INFORMATION: /standard_name= "Constitutional promoter"
/label= Cp44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CATCGGGTAG TTTATTCTTG ACAATTAAGT AGAGCCTGAT ATAATAGTTC AGTACTGTT

59

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..59

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Constitutional promoter"
/label= Cp5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CATGGGGGAG TTTATTCTTG ACATCATCTT CGTAGCCTGG TATACTACAT GAGTATGTT

59

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION: 4..60
(D) OTHER INFORMATION: /standard_name= "Constitutional
promoter"
/label= Cp6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CATGTGGGAG TTTATTCTTG ACACAGATAT TTCCGGATGA TATAATAACT GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION: 4..60
(D) OTHER INFORMATION: /standard_name= "Constitutional
promoter"
/label= Cp7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TATGCGGTAG TTTATTCTTG ACATGACGAG ACAGGTGTGG TATAATGGGT CTAGATTAGG 60

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:
(A) NAME/KEY: promoter

(B) LOCATION:4..60
(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CATTCTTTAG TTTATTCTTG ACAAACGTAT TGAGGACTGA TATAATAGGT GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter
(B) LOCATION:4..60
(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CATAGTCTAG TTTATTCTTG ACACGCGGTC CATTGGCTGG TATAATAATT TAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter
(B) LOCATION:8..177
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION:/evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAATTCGTGA CTCAAACGGG TGGTCGACGG GTGGTTCCAA TTAATTGGCG TCCCTCTTAT 60
AAAGGCGAGG GTACGTGCGA CAATTGGTAG AGCGAGCGGG GCTCTTAAGT GCAAGTGACT 120
GCGAACATTT TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC 177

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..181
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard name= "Yeast promoter"
/label= Yp112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAATTCGTGA CTCACGGCAT CTGATGGTTG ACCATAGTCA GGAACATTGT GCTGGAGTTC 60
CTTGAGGAAT GAGTTATAAA ATGGGAGGTT GCGGCTAATG CCAGGCAGGA GAGGAACCCT 120
CTTAAGTGCA AGTGACTGCA AACATTTTTT TCGTTTGTTG AATCGCTACC AATCATGGAT 180
CC 182

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..181
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GAATTCGTGA CTCACTAGGC AGGTCACGTT GGCTCTTCGC GGCGCAGGTT CGTATGCCGC 60
GCCGCCAGGG GCTTTATAAA GTCGTCCTG GGTACAGTTG GGATGGCTCC ACGTTTCGGC 120
TCTTAAGTGC AAGTGACTGC GAACATTTTCG TTTGTTAGAA TAATTCAAGA ATCGCTACCA 180
ATCATGGATC C 191

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Saccharomyces cerevisiae*
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION: 8..167
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GAATTCGTGA CTCAGGGCCG TACTAAGTAG CTTTCGTATG CTATGCGGGG TTTTATAAAT 60
CTTTGGGCCA TGGTCTTGCT GGAAAACACC TCTCTTAAGT GCAAGTGA CTGCAACATTT 120
TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC 167

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..191

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GAATTCGTGA CTCACCGCTC GGGTGCAGGG CCAAGGCGGC GGAATGTGCG GGGCGTTCTA	60
GCGCAATCGG GGTATAAATT TATAAGGAGG CTGCGGGTGC TAGTTTGTCT AGTTTGACTC	120
TTAAGTGCAA GTGACTGCGA ACATTTTTCG TTTGTTAGAA TAATTCAAGA ATCGCTACCA	180
ATCATGGATC C	191

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..190

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GAATTCGTGA CTCAGGATTA GCTATGCCGG TTGGGATAAG CGAACAACTG GAGGTGAGAA	60
GCTTTTTGTC AGAATATAAA CCCGTTAGTC AGGGTTTGGT GGGATAGGGG GTACTGTACC	120
TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT	180
ACCAATCATG GATCC	195

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 179 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Saccharomyces cerevisiae*
- (ix) FEATURE:
 (A) NAME/KEY: promoter
 (B) LOCATION: 8..179
 (C) IDENTIFICATION METHOD: experimental
 (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
 /standard_name= "Yeast promoter"
 /label= Yp183
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GAATTCGTGA CTCACTAAGG GTTCGCCATT AACAGAATCG CTGGTAGAAC ATCGGTTAGTT 60
AGGCACCCGA GTATAAACAG GCGGACCCCT CACGGATATC AGCTGATAGT GCGAGCCTCA 120
ATGCGAACAT TTTTTCGTT TGTTAGAATA ATTCAAGAAT CGCTACCAAT CATGGATCC 179

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Saccharomyces cerevisiae*
- (ix) FEATURE:
 (A) NAME/KEY: promoter
 (B) LOCATION: 8..190
 (C) IDENTIFICATION METHOD: experimental
 (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
 /standard_name= "Yeast promoter"
 /label= Yp190
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

GAATTCGTGA CTCAGTATCC ACGGGTGTTT GAGGGCTGGT CGCAGGTTAG CAGGCGAGGG 60
CGGGTGGTTA CGGCTATAAA TGAGTGTTTG CAGCCGGGTA CGGGCGTACG AGTAGTGATC 120

TCTTAAATGC AAGTGACTGC GAACATTTTT TTCGTTTGT AGAATAATTC AAGAATCGCT 180
ACCAATCATG GATCC 195

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Saccharomyces cerevisiae*
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION: 8..189
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yest promoter"
/label= Yp191
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAATTCGTGA CTCAATGCTG CGGGCGGCAG GAGTCTGGTG TAACTTCCCA TTTTGAGTGA 60
AAGACAGACC ATCTATAAAC ATTTGGTGGG CAAAGTGGCC TGGCGGATTT GTTTGGACTC 120
TTAAGTGAAA GTGACTGCGA ACATTTTTTTT CGTTTGTTAG AATAATTCAA GAATCGCTAC 180
CAATCATGGA TCC 193

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Saccharomyces cerevisiae*
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION: 8..166
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/standard_name= "Yeast promoter"
/label= Yp192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GAATTCGTGA CTCACTTAAG GCTACTGCGG AAGTTTAGAT CTAAGGTCGG AAATAATTTA 60
GAAAATTACG ACATTATAAA TAGCGGAGAG GCCAGGTGAT GGGCACCATT GTGGGGGGGC 120
TCTTAATTGT TAGAATAATT CAAGAATCGC TACCAATCAT GGATCC 166

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..190
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GAATTCGTGA CTCAGTCGCC CGCAAGATGG GATGGTGCAT TTAAACACC CGAATTATAC 60
TCGTCAACTT ATAGTATAAA CGGAACGCGA CGATACGTTC TAGTTTTTCGG CGAAGTCGAC 120
TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT 180
ACCAATCATG GATCC 195

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..183
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```
GAATTCGTAC TCACGACAGC GTTATGACTT CGAGGACCAG CTACTTCCGG TCGCGTACTA      60
GTTTTTACCT GTATAAACTT TGCTACCGCT GGGCCTTGGT GGTGCTGTCC CGCTCTTAAG      120
TGCAAGTGAC TGCGAACATT TTTTTCGTTT GTTACAATAA TTCAAGAATC GCTACCAATC      180
ATGGATCC                                     188
```

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..190
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```
GAATTCGTGA CTAAATGGAT AAGGTTATCG CCATCACGGA GTCTTCTCTC ACGTCTGGAG      60
CAGAGGCTAG ACCTTATAAA TTATACATGG TGGGAGAGGC GATAGTCTTT AGAGACGTGC      120
TCTTAAGTGC AAGTGACTGC GAACATTTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT      180
ACCAATCATG GATCC                                     195
```

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..184

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/standard_name= "Yeast promoter"

/label= Yp68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GAATTCGTGA CTCACAAGAA TGTGGGCGGG TCGTTAACT GAGCCTGGAC ACCTTGGCTG	60
CGTCGCTTTC GTATAAAGAT CTTAGAGCTG TGGAGTCTGG GTCGAGTGGC CAGCTCTTAA	120
ATGCAAGTGA CTGCGAACAT TTTTTCGTT TGTTAGAATA ATTCAAGAAT CGCTACCAAT	180
CATGGATCC	189

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..190

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/standard_name= "Yeast promoter"

/label= Yp89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GAATTCGTGA CTCACTCGGA AGATTGGGTT TACGATTAGG ATGGCGCGGC AGAACCGGGG	60
GGGATTCCCT TCTATATAAA GGGTTCCGAT ACTACGTGCT GCGGACGGCC GATCGAGTTA	120
TCTTAAGTGC AAGTGACTGC GAAAATTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT	180

195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- ```
(A) NAME/KEY: promoter
(B) LOCATION:8..171
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION:/evidence= EXPERIMENTAL
 /standard_name= "Yeast promoter"
 /label= Yp96
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGTGA | CTCATCTAGT | GAGAGGAGCC | GTGGTATCTT | GTGTCACCAC | CAGGGGAAAA | 60  |
| TAATGGCAGG | GGTGTATAAA | TGGTCGAGTA | GTCGCGACCC | ACGCTGCAAG | GCAAGGAACT | 120 |
| CTTAAATTTT | TTTCGTTTGT | TAGAATAATT | CAAGAATCGC | TACCAATCAT | GGATCC     | 176 |